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PATENT
Attorney Docket No.: 17726A-000420US

Assistant Commissioner for Patents
Washington, D.C. 20231

On February 13, 2007

TOWNSEND and TOWNSEND and CREW LLP

By: [Signature]

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

LEE *et al.*

Application No.: 10/028,726

Filed: December 21, 2001

For: PRODUCTS AND METHODS FOR
CONTROLLING THE SUPPRESSION
OF THE NEOPLASTIC PHENOTYPE

Examiner: Not yet assigned

Art Unit: 1633

COMMUNICATION UNDER

37 C.F.R. §§ 1.821-1.825

AND

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825, mailed December 13, 2002, Applicants submit that the computer-readable form in the instant application is identical with that filed in Application No. 08/472,760, filed November 27, 1996. In accordance with 37 C.F.R. § 1.821(e), please use the computer-readable form filed in Application No. 08/472,760 as the computer-readable form for the instant application. A paper copy of the last filed Sequence Listing from Application No. 08/472,760 is submitted herewith. The information in the paper copy of the Sequence Listing is identical to that which is in the computer readable form, as required under 37 C.F.R. § 1.821(f).

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It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for the computer-readable form that will be used for the instant application.

Please amend the specification in adherence with 37 C.F.R. §§ 1.821-1.825 as follows.

In the Specification:

Please replace paragraph [152] beginning at page 27, line 15, with the following:

[152] --The hypothetical protein predicted from the nucleotide sequence was expected to have MW about 106 kD. The immunoprecipitated protein has a MW about 110-114 kD. The complete RB protein amino acid sequence (SEQ ID NO:2) is illustrated in Table 1. This complete sequence obtained from the newly reconstructed clone which contains the most 5' end stretch missing in the original cDNA clone Science, 235:1394-1399 (1987).

TABLE 1

[M]PPKTPRKTAATAAAAAAEPPAPPPPPPPPEEDPE	(34)
QDSGPEDLPLVRLEFEETEEDFTALCQKLKIPDHVRERA	(74)
WLTWEKVSSVDGVLGGYIQKKKELWGICIFIAAVDLDE[M]S	(114)
FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK	(154)
YDVLFAFSLKERTCELIYLTQPSSSISTEINSALVLKVS	(194)
WITFLLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML	(234)
LKEPYKTAVIPINGSRTPRRGQMRSAARIAKQLENDTRII	(274)
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	(314)
ENLSKRYEEIYLKNKDLDARLFLDHDKTLQTDSDSFETQ	(354)
RTPRKSNLDEEVNVIPHTPVRTVMNTIQQLMMILNSASD	(394)
QPSENLISYFNNCTVNPKESILKRVKDIFYIFKEKFAKAV	(434)
GQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFS	(474)
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSF	(514)
PWILNVNLKAFDFYKVIESFIKAEGNLTREMIKHLERCE	(554)
HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL	(594)
PLQNNHTAADMYLSPVRSPKKKGSTTRVNSTANAETQATS	(634)
AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP	(674)
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV	(714)
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIV	(754)
FYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPS	(794)
SPLRIPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVS	(834)
IGESFGTSEKFQKINQMCNSDRVLKRSAEGSNPPKPLKK	(874)
LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ	(914)
KMNDSDMDTSNKEEK	(928)

single-letter abbreviations for the amino acid residues are:
 A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;
 I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;
 R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.--

Please replace paragraph [153] beginning at page 27, line 15, with the following:

[153] --The amino acid sequence (Table 1; SEQ ID NO:2) is written in the abbreviation code recognized in the art. Single-letter abbreviations for the amino acid residues are: A = Alanine, C = Cysteine, D = Aspartic acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N =

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Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophane and Y = Tyrosine.--

Please replace paragraph [225] beginning at page 27, line 15, with the following:

[225] --Pending U.S. patent application Serial No. 108,748 discloses and claims the RB gene and its clone. The RB gene and its clone had the nucleotide and amino acid sequences sequence depicted in Table 4 Table 2 (SEQ ID NOS:1 and 2).

TABLE 4

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGC GCGC GCGTCGTCCT CCGGGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	

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ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
140 145 150 155	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
160 165 170	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	699
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
175 180 185	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
190 195 200	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
205 210 215	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
220 225 230 235	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	891
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
240 245 250	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
255 260 265	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
270 275 280	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
285 290 295	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
300 305 310 315	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
320 325 330	

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GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
335 340 345	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
350 355 360	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
365 370 375	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380 385 390 395	
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400 405 410	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415 420 425	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430 435 440	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445 450 455	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460 465 470 475	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480 485 490	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495 500 505	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510 515 520	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525 530 535	

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GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560 565 570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575 580 585	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
590 595 600	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
605 610 615	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
620 625 630 635	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
640 645 650	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
655 660 665	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
670 675 680	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
685 690 695	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
700 705 710 715	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
720 725 730	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
735 740 745	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2427

Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	
750						755						760				
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	
765						770						775				
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	
780						785						790				795
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	
800						805						810				
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	
815						820						825				
AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2667
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	
830						835						840				
AAG	TTC	CAG	AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	2715
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	
845						850						855				
AAA	AGA	AGT	GCT	GAA	GGA	AGC	AAC	CCT	CCT	AAA	CCA	CTG	AAA	AAA	CTA	2763
Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	
860						865						870				875
CGC	TTT	GAT	ATT	GAA	GGA	TCA	GAT	GAA	GCA	GAT	GGA	AGT	AAA	CAT	CTC	2811
Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	
880						885						890				
CCA	GGA	GAG	TCC	AAA	TTT	CAG	CAG	AAA	CTG	GCA	GAA	ATG	ACT	TCT	ACT	2859
Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	
895						900						905				
CGA	ACA	CGA	ATG	CAA	AAG	CAG	AAA	ATG	AAT	GAT	AGC	ATG	GAT	ACC	TCA	2907
Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	
910						915						920				
AAC	AAG	GAA	GAG	AAA	TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT											2962
Asn	Lys	Glu	Glu	Lys												
925																
GGATTCATTG TCTCTCACAG ATGTGACTGT AT																2994

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TABLE 4

TTCCGCTTTT TCTCAGCGGA CGTTGAAATT ATTTTGTAA CCGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGCGCGC GCGTCTCTCT CCCCCGGGCT CCTCCACAGC TCGCTGGCTC	120
CCGCGCGCGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT CCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCG TAG GAG GAC CCA GAG CAG CAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC CTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT CCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA CTT TCA TCT CTC GAT GCA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	
ATA GAA ATC AGT CTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTC TTG AAG AAG TAT	603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
140 145 150 155	
GAT GTA TTG TTT GCA CTC TTC ACC AAA TTG GAA AGC ACA TGT GAA CTT	651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
160 165 170	

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ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	699
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
175 180 185	
GCA TTG GTC CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
190 195 200	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
205 210 215	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTC CTC	843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
220 225 230 235	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GCT TCA CCT CGA	891
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
240 245 250	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
255 260 265	
GAA AAT GAT ACA ACA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
270 275 280	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
285 290 295	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
300 305 310 315	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
320 325 330	
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
335 340 345	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
350 355 360	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
365 370 375	

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AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380 385 390 395	
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400 405 410	
AAA GAA AGT ATA CTG AAA ACA GTG AAG CAT ATA GCA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415 420 425	
GAG AAA TTT GCT AAA GCT CTG GCA CAG GGT TCT CTC GAA ATT GGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430 435 440	
CAG CGA TAC AAA CTT CGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445 450 455	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460 465 470 475	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG CCG TGC GCT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480 485 490	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495 500 505	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510 515 520	
AAA GCC TTT CAT TTT TAC AAA CTG ATC GAA AGT TTT ATC AAA GCA GAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525 530 535	
GCC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560 565 570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GCA CCA ACT GAT CAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575 580 585	

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~~TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA~~ 1947
~~Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala~~
~~590 595 600~~

~~GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT~~ 1995
~~Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr~~
~~605 610 615~~

~~ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC~~ 2043
~~Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala~~
~~620 625 630 635~~

~~TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT~~ 2091
~~Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr~~
~~640 645 650~~

~~AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA~~ 2139
~~Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu~~
~~655 660 665~~

~~CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT~~ 2187
~~Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu~~
~~670 675 680~~

~~TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT~~ 2235
~~Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His~~
~~685 690 695~~

~~TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG~~ 2283
~~Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys~~
~~700 705 710 715~~

~~AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA CCA TAC AAG GAT CTT~~ 2331
~~Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu~~
~~720 725 730~~

~~CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG~~ 2379
~~Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu~~
~~735 740 745~~

~~GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA~~ 2427
~~Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg~~
~~750 755 760~~

~~CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG~~ 2475
~~Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu~~
~~765 770 775~~

~~TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA~~ 2523
~~Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser~~
~~780 785 790 795~~

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CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
      800                      805                      810

CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
      815                      820                      825

AGA TCA AGA ATC TTA GTA TCA ATT GGT CAA TCA TTC GGG ACT TCT GAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
      830                      835                      840

AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC ACC GAC CGT CTG CTC 2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
      845                      850                      855

AAA AGA ACT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
      860                      865                      870                      875

CGC TTT GAT ATT GAA GGA TCA GAT CAA GCA GAT GGA AGT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
      880                      885                      890

CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
      895                      900                      905

CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
      910                      915                      920

AAC AAG CAA GAG AAA TCAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT 2962
Asn Lys Glu Glu Lys
      925

GGATTCATTG TCTCTCACAG ATGTGACTGT AT 2994
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Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.

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In the Claims:

Please amend claims 35, 39 and 40 as follows:

1. (Original) A method of controlling cancer suppression in a mammal having a cancer suppressing gene, comprising the steps of:
making a substantially duplicated genetic material corresponding to the genetic material of said gene, the substantially duplicated material selected from the group consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof; and
interchanging said duplicated genetic material and the cancer suppressing gene of the mammal.
2. (Original) A method of claim 1, wherein before said making a substantially duplicated genetic material, determining the chromosomal location of said cancer suppressing gene of the mammal.
3. (Original) A method of claim 1, wherein after said making a substantially duplicated genetic material, detecting the presence or absence of an inactive cancer suppressing gene of a tissue sample of the mammal to determine whether or not the tissue sample cancer suppressing gene is defective or absent.
4. (Original) A method of claim 3, wherein in response to a determination that the tissue sample cancer suppressing gene is either defective or absent, replacing a cancer suppressing gene of the mammal with its clone.

6. (Original) A method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by:

7. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme immunoassay techniques.

9. (Original) The method of claim 5, wherein the cancer suppressing gene is the RB gene and the protein product is ppRB¹¹⁰.

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10. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for therapeutic purposes.

11. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for facilitating the testing of the carcinogenicity of environmental influences.

12. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined by chromosome walking.

13. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined through organic markers.

14. (Original) A method of claim 2, wherein:
said chromosomal location of said cancer suppressing gene is determined by testing genes of a chromosome for phenotypic expression;
determining one of the genes of said chromosome to be a marker gene; and
using chromosomal walking techniques to locate a cancer suppressing gene.

15. (Original) An animal genetically altered so as to have the allele of at least one cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof.

16. (Original) An animal of claim 15, wherein said defective allele is selected from the group consisting of defective alleles of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

17. (Original) An animal of claim 15, wherein said allele contains a DNA fragment having at least one defective nucleotide sequence.

18. (Original) An animal of claim 15, wherein said defective allele contains a DNA fragment having at least one defective RB nucleotide sequence.

19. (Original) The animal of claim 15, wherein said animal is a mouse.

20. (Original) A method for determining the carcinogenicity of suspected environmental influences, using the animal of claim 14, comprising the steps of:
exposing said animal to a suspected environmental influence;
observing the animal for the phenotypic expression of cancer; and
determining carcinogenicity of the suspected environmental influence in response to observing a phenotypic expression of cancer in the animal.

21. (Original) A method of claim 20, wherein said exposing includes exposing to a source of radiation.

22. (Original) A method of claim 20, wherein said exposing includes exposing to tobacco combustion products.

23. (Original) A method of claim 20, wherein said exposing includes exposing to food additives.

24. (Original) A method of claim 20, wherein said exposing includes exposing to artificial substances.

25. (Original) A method of claim 20, wherein said observing includes examining the animal for tumor development.

26. (Original) A method of claim 25, wherein in response to the formation of a tumor in the animal, analyzing the tumor for the presence of cancer cells.

27. (Original) A method of making the animal of claim 15, comprising:
using at least one allele of an animal cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof;

mutating at least one animal cell with said allele to form a mutated cell;
introducing said mutated cell into an animal blastocyst;
permitting growth of the blastocyst for a given period of time sufficient to incorporate said allele into its cells; repressing genetic recombinations within said cells;
transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal for giving birth subsequently to an animal bearing said allele;

breeding said animal to reproduce additional animals; and
selecting the animal of claim 14 from said additional animals by determining the presence therein of the said allele.

33. (Original) A pharmaceutical composition of claim 31, wherein the active ingredient for each of said gene is selected from the group consisting of cDNA of said gene, fragments of said cDNA, homologues thereof and mixtures thereof.

34. (Original) A pharmaceutical composition of claim 32, wherein the cancer suppressing gene is isolated from human chromosome 13 region 13q14.

35. (Currently amended) A pharmaceutical composition of claim 31, wherein the cancer suppressing gene and its clone each has the following nucleotide sequence comprising SEQ ID NO:1.:

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TTCCCGTTTT TCTCAGGGGA CCTTGAAATT ATTTTGTAA CCGGAGTCGG GAGAGGACGG      60
GGCGTGCCCC GCGTGCGGCG GCGTCGTCTT CCGCGGCGCT CCTCCACAGC TCGCTGGCTC      120
CGCGCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC      219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25
CCT CCG TAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT      267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG      363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GCA GTA TTG GGA GGT TAT      411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA      459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120
ATA GAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

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~~ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTC TTG AAG AAG TAT~~ 603
~~Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr~~
~~140 145 150 155~~

~~GAT GTA TTC TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT~~ 651
~~Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu~~
~~160 165 170~~

~~ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT~~ 699
~~Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser~~
~~175 180 185~~

~~GCA TTG GTG CTA AAA GTT TCT TGC ATC ACA TTT TTA TTA CCT AAA GGG~~ 747
~~Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly~~
~~190 195 200~~

~~GAA GTA TTA CAA ATG GAA GAT GAT CTG CTG ATT TCA TTT CAG TTA ATG~~ 795
~~Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met~~
~~205 210 215~~

CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
220 225 230 235

~~AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA~~ 891
~~Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg~~
~~240 245 250~~

~~ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CCG ATA GCA AAA CAA CTA~~ 939
~~Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu~~
~~255 260 265~~

~~GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT~~ 987
~~Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys~~
~~270 275 280~~

~~AAT ATA GAT CAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT~~ 1035
~~Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe~~
~~285 290 295~~

~~ATC AAT TCT CTT CGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA 1083~~
~~Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu~~
~~300 305 310 315~~

~~AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA~~ 1131
~~Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu~~
~~320 325 330~~

~~GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179~~
~~Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser~~
~~335 340 345~~

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~~ATA CAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT~~ 1227
~~Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp~~
~~350 355 360~~

~~GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG~~ 1275
~~Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met~~
~~365 370 375~~

~~AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA~~ 1323
~~Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln~~
~~380 385 390 395~~

~~CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA~~ 1371
~~Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro~~
~~400 405 410~~

~~AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GCA TAC ATC TTT AAA~~ 1419
~~Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys~~
~~415 420 425~~

~~GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT CTC GAA ATT GGA TCA~~ 1467
~~Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser~~
~~430 435 440~~

~~CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC~~ 1515
~~Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser~~
~~445 450 455~~

~~ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA~~ 1563
~~Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys~~
~~460 465 470 475~~

~~CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT~~ 1611
~~Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu~~
~~480 485 490~~

~~GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT~~ 1659
~~Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp~~
~~495 500 505~~

~~TCT CGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA~~ 1707
~~Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu~~
~~510 515 520~~

~~AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA~~ 1755
~~Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu~~
~~525 530 535~~

~~GCC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT~~ 1803
~~Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His~~
~~540 545 550 555~~

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~~CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT~~ 1851
~~Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp~~
~~560 565 570~~

~~CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA~~ 1899
~~Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu~~
~~575 580 585~~

~~TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA~~ 1947
~~Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala~~
~~590 595 600~~

~~GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT~~ 1995
~~Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr~~
~~605 610 615~~

~~ACG CGT GTA AAT TCT ACT GCA AAT GCA CAG ACA CAA GCA ACC TCA GCC~~ 2043
~~Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala~~
~~620 625 630 635~~

~~TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT~~ 2091
~~Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr~~
~~640 645 650~~

~~AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA~~ 2139
~~Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu~~
~~655 660 665~~

~~CGC CTT CTC TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT~~ 2187
~~Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu~~
~~670 675 680~~

~~TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGC CAT~~ 2235
~~Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His~~
~~685 690 695~~

~~TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG~~ 2283
~~Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys~~
~~700 705 710 715~~

~~AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT~~ 2331
~~Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu~~
~~720 725 730~~

~~CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG~~ 2379
~~Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu~~
~~735 740 745~~

~~GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA~~ 2427
~~Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg~~
~~750 755 760~~

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~~CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG~~ 2475
~~Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu~~
~~765 770 775~~

~~TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA~~ 2523
~~Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser~~
~~780 785 790 795~~

~~CCC TTA CGG ATT CCT GCA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT~~ 2571
~~Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser~~
~~800 805 810~~

~~CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA~~ 2619
~~Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro~~
~~815 820 825~~

~~AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GCG ACT TCT GAG~~ 2667
~~Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu~~
~~830 835 840~~

~~AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC~~ 2715
~~Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu~~
~~845 850 855~~

~~AAA AGA AGT GCT CAA GCA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA~~ 2763
~~Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu~~
~~860 865 870 875~~

~~CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC~~ 2811
~~Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu~~
~~880 885 890~~

~~CCA CGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT~~ 2859
~~Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr~~
~~895 900 905~~

~~CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA~~ 2907
~~Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser~~
~~910 915 920~~

~~AAC AAC CAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT~~ 2962
~~Asn Lys Glu Glu Lys~~
~~925~~

~~GGATTCATTG TCTCTCACAG ATGTGACTGT AT~~ 2994

36. (Original) A pharmaceutical composition of claim 32, wherein said RB cDNA fragment is selected from the group consisting of RB-1, RB-2, RB-5, y79R8 and mixtures thereof.

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37. (Original) A pharmaceutical composition of claim 32, wherein a resulting mRNA transcript of said RB cDNA fragment has 4.6 kb.

38. (Original) A pharmaceutical composition of claim 37, wherein the cloned genomic DNA has at least 27 exons.

39. (Currently amended) A pharmaceutical composition of claim 30, wherein the cloned RB cDNA transcribes into mRNA which translates in protein having an amino acid sequence comprising SEQ ID NO:2:

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MPPKTPRKTAATAAAAAAEPAPPPPPPPPEEDPE ( 34)
QDSCPEDLPLVRLEFEETEEDFTALCQKLKIPDHVRERA ( 74)
WLTWEKVSSVDCVLGCIYQKKKELWGCICIFIAAVDLDEMIS (114)
FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK (154)
YDVLFALEFSKLEERTCELIYLTQPSSSISTEINSALVLKVS (194)
WITFLLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML (234)
LKEPYKTAVIPINGSPRTPRRGQMRSAARIAKQLENDTRI (274)
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV (314)
ENLSKRYEEIYLNKNDLDARLFLDHDKTLQTDSDISFETQ (354)
RTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSASD (394)
QPSENLI SYFNCTVNPKE SILKRVKDICYIFKEKFAKAV (434)
GQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFS (474)
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSCTDLSF (514)
PWILNVNLKAFDFYKVIESFIKAECNLTREMIKHLERCE (554)
HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL (594)
PLQNNHTAADMYLSPVRSPPKKKGSTTRVNSTANAETQATS (634)
AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP (674)
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV (714)
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIV (754)
FYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPS (794)
SPLRIPGCNIYISPLKSPYKISEGLPTPTKMTPRSRILVS (834)
IGESFGTSEKFQKINQMVCSNDRVLKRSAGCSNPPKPLKK (874)
LRFDIEGSDEADGSKHLPGESKFQQLAEMTSTRTRMQKQ (914)
KMND SMDTSNKEEK (928)

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single letter abbreviations for the amino acid residues are:
A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;

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I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;
R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

40. (Currently amended) A DNA nucleotide sequence comprising SEQ

ID NO:1.:

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TTCCGGTTTT TCTCAGGGGA CCTTGAAATT ATTTTGTAA CCGGAGTCCG GAGAGGACGG      60
GGCGTGCCCC GCCTGCGCGC GCGTCGTCTT CCCCAGCGCT CCTCCACAGC TCGCTGGCTC      120
CCGCGCGCGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG CCC CCC      171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC CCC CCC GCT CCC CCC GCG GAA CCC CCG GCA CCG CCG CCG CCC      219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro
15 20 25
CCT CCG TAG GAG GAC CCA GAG CAG GAC AGC GCG CCG GAG GAC CTC CCT      267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA CCT TGC      363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT      411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAC AAA AAG GAA CTG TCG GCA ATC TGT ATC TTT ATT GCA GCA      459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA CAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

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~~ACC AGT ACC AAA GTT CAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT~~ 603
~~Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr~~
~~140 145 150 155~~

~~GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT~~ 651
~~Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu~~
~~160 165 170~~

~~ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT~~ 699
~~Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser~~
~~175 180 185~~

~~GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GCG~~ 747
~~Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly~~
~~190 195 200~~

~~GAA GTA TTA CAA ATG CAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG~~ 795
~~Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met~~
~~205 210 215~~

~~CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC~~ 843
~~Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu~~
~~220 225 230 235~~

~~AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CCA~~ 891
~~Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg~~
~~240 245 250~~

~~ACA CCC AGG CGA CGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA~~ 939
~~Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu~~
~~255 260 265~~

~~GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT~~ 987
~~Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys~~
~~270 275 280~~

~~AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT~~ 1035
~~Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe~~
~~285 290 295~~

~~ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA~~ 1083
~~Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu~~
~~300 305 310 315~~

~~AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA~~ 1131
~~Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu~~
~~320 325 330~~

~~GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT~~ 1179
~~Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser~~
~~335 340 345~~

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~~ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT~~ 1227
~~Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp~~
~~350 355 360~~

~~GAA GAG CTC AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG~~ 1275
~~Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met~~
~~365 370 375~~

~~AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA CCA AGT GAT CAA~~ 1323
~~Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln~~
~~380 385 390 395~~

~~CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA~~ 1371
~~Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro~~
~~400 405 410~~

~~AAA GAA ACT ATA CTG AAA AGA GTG AAG CAT ATA GGA TAC ATC TTT AAA~~ 1419
~~Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys~~
~~415 420 425~~

~~GAG AAA TTT CCT AAA CCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA~~ 1467
~~Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser~~
~~430 435 440~~

~~CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC~~ 1515
~~Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser~~
~~445 450 455~~

~~ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA~~ 1563
~~Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys~~
~~460 465 470 475~~

~~CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC CCT CTT~~ 1611
~~Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu~~
~~480 485 490~~

~~GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT~~ 1659
~~Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp~~
~~495 500 505~~

~~TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA~~ 1707
~~Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu~~
~~510 515 520~~

~~AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA~~ 1755
~~Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu~~
~~525 530 535~~

~~GCG AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT~~ 1803
~~Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His~~
~~540 545 550 555~~

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~~CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT~~ 1851
~~Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp~~
~~560 565 570~~

~~CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA~~ 1899
~~Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu~~
~~575 580 585~~

~~TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA~~ 1947
~~Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala~~
~~590 595 600~~

~~GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT~~ 1995
~~Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr~~
~~605 610 615~~

~~ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC~~ 2043
~~Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala~~
~~620 625 630 635~~

~~TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT~~ 2091
~~Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr~~
~~640 645 650~~

~~AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA~~ 2139
~~Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu~~
~~655 660 665~~

~~CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT~~ 2187
~~Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu~~
~~670 675 680~~

~~TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT~~ 2235
~~Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His~~
~~685 690 695~~

~~TTG GAC CAA ATT ATG ATG TCT TCC ATG TAT CGC ATA TGC AAA GTG AAG~~ 2283
~~Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys~~
~~700 705 710 715~~

~~AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT~~ 2331
~~Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu~~
~~720 725 730~~

~~CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT CTT TTG ATC AAA GAA GAG~~ 2379
~~Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu~~
~~735 740 745~~

~~GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA~~ 2427
~~Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg~~
~~750 755 760~~

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~~CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG~~ 2475
~~Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu~~
~~765 770 775~~

~~TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA~~ 2523
~~Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser~~
~~780 785 790 795~~

~~CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT~~ 2571
~~Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser~~
~~800 805 810~~

~~CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA~~ 2619
~~Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro~~
~~815 820 825~~

~~AGA TCA ACA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG~~ 2667
~~Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu~~
~~830 835 840~~

~~AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC~~ 2715
~~Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu~~
~~845 850 855~~

~~AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA~~ 2763
~~Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu~~
~~860 865 870 875~~

~~CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC~~ 2811
~~Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu~~
~~880 885 890~~

~~CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG CCA GAA ATG ACT TCT ACT~~ 2859
~~Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr~~
~~895 900 905~~

~~CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA~~ 2907
~~Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser~~
~~910 915 920~~

~~AAC AAG CAA GAG AAA TCAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT~~ 2962
~~Asn Lys Glu Glu Lys~~
~~925~~

~~GGATTCATTG TCTCTCACAG ATGTGACTGT AT~~ 2994

41. (Original) A method of therapeutically treating inactive, mutative or absent cancer suppressing genes comprising:

treating said inactive, mutative or absent cancer suppressing genes with at least a portion of intact cancer suppressing genes.

42. (Original) A method of claim 41, wherein said cancer suppressing genes are each a substance selected from the groups consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures thereof.

43. (Original) A method of claim 41, wherein said treating includes:
treating said inactive, mutative or absent cancer suppressing gene with a substance selected from the group consisting of an RB gene, a portion of said gene, or a mixture thereof.

44. (Original) A method of claim 43, wherein said portion is selected from the group consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.

45. (Original) The method of claim 41, wherein the intact cancer suppressing gene, or portion thereof, is delivered to the site of a tumor by means of a retrovirus.

46. (Original) A method of claim 41, wherein the intact cancer suppressing gene, or a portion thereof, is delivered to the site of a tumor by a liposome.

47. (Original) A method of claim 41, wherein the location of said cancer suppressing gene is determined by utilizing a genetic marker.

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47. (Previously added) A method of suppressing the neoplastic phenotype of a cancer cell, the method comprising contacting the cell with a nucleic acid encoding a full length, wild type retinoblastoma protein.

REMARKS

The amendments to the nucleotide sequence in "TABLE 4" and claims 35 and 40 correct errors of a typographical nature made without deceptive intent. The codons at nucleotide positions 223-225 (CCT), encoding "Pro", and 226-228 (GAG), encoding "Glu", were present in the original sequence from informal Figure 9 of the parent application, 08/472,760, filed November 27, 1996, a copy of which is enclosed for the convenience of the Examiner. These codons were inadvertently changed to "CCG" and "TAG" in the present application. That this is inadvertent error is supported by the fact that, under "TAG" at positions 226-228, which encodes a stop codon, the originally-encoded amino acid "E" (Glu) appears in "TABLE 4" of the Specification submitted on December 21, 2001, and "Glu" again appears in the Substitute Specification submitted April 30, 2002, in response to the Notice to File Corrected Application Papers, mailed January 31, 2002.

The Sequence Listing submitted for Application No. 08/472,760, filed November 27, 1996, does not contain these inadvertent errors and, thus, the amendments to the Specification and Claims now seek to conform to the nucleotide sequence present in the Sequence Listing of the parent application.

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. The information contained in the computer readable form of Application No. 08/472,760 was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy, a copy of which is enclosed for the convenience of the Examiner. This amendment contains no new matter.